

(1) GENERAL INFORMATION

- (2) INFORMATION FOR SEQ ID NO:1:

- 53

PF-0181 US

Met Leu Ala Arg Ala Ala Arg Gly His Trp Gly Pro Phe Ala Glu Gly
 1 5 10 15
 Leu Ser Thr Gly Phe Trp Pro Arg Ser Gly Arg Ala Ser Ser Gly Leu
 20 25 30
 Pro Arg Asn Thr Val Val Leu Phe Val Pro Gln Gln Glu Ala Trp Val
 35 40 45
 Val Glu Arg Met Gly Arg Phe His Arg Ile Leu Glu Pro Gly Leu Asn
 50 55 60
 Ile Leu Ile Pro Val Leu Asp Arg Ile Arg Tyr Val Gln Ser Leu Lys
 65 70 75 80
 Glu Ile Val Ile Asn Val Pro Glu Gln Ser Ala Val Thr Leu Asp Asn
 85 90 95
 Val Thr Leu Gln Ile Asp Gly Val Leu Tyr Leu Arg Ile Met Asp Pro
 100 105 110
 Tyr Lys Ala Ser Tyr Gly Val Glu Asp Pro Glu Tyr Ala Val Thr Gln
 115 120 125
 Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys Leu Ser Xaa Asp
 130 135 140
 Lys Val Phe Arg Glu Arg Glu Ser Leu Asn Ala Ser Ile Val Asp Ala
 145 150 155 160
 Ile Asn Gln Ala Ala Asp Cys Trp Gly Ile Arg Cys Leu Arg Tyr Glu
 165 170 175
 Ile Lys Asp Ile His Val Pro Pro Arg Val Lys Glu Ser Met Gln Met
 180 185 190
 Gln Val Glu Ala Glu Arg Arg Lys Arg Ala Thr Val Leu Glu Ser Glu
 195 200 205
 Gly Thr Arg Glu Ser Ala Ile Asn Val Ala Glu Gly Lys Lys Gln Ala
 210 215 220
 Gln Ile Leu Ala Ser Glu Ala Glu Lys Ala Glu Gln Ile Asn Gln Ala
 225 230 235 240
 Ala Gly Glu Ala Ser Ala Val Leu Ala Lys Ala Lys Ala Lys Ala Glu
 245 250 255
 Ala Ile Arg Ile Leu Ala Ala Ala Leu Thr Gln His Asn Gly Asp Ala
 260 265 270
 Ala Ala Ser Leu Thr Val Ala Glu Gln Tyr Val Ser Ala Phe Ser Lys
 275 280 285
 Leu Ala Lys Asp Ser Asn Thr Ile Leu Leu Pro Ser Asn Pro Gly Asp
 290 295 300
 Val Thr Ser Met Val Ala Gln Ala Met Gly Val Tyr Gly Ala Leu Thr
 305 310 315 320
 Lys Ala Pro Val Pro Gly Thr Pro Asp Ser Leu Ser Ser Gly Ser Ser
 325 330 335
 Arg Asp Val Gln Gly Thr Asp Ala Ser Xaa Asp Glu Glu Leu Asp Arg
 340 345 350
 Val Lys Met Ser
 355

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| GGCTTCTGGG | AGCNACCGCT | CCGCTCGTCT | CGTTGGTTCC | GGAGGTGCGT | GCGGCGGTGG | 60 |
| GAAATGCTGG | CGCGCGCGGC | GCGGGGGCAC | TGGGGCCCTT | TTGCTGAGGG | GCTCTCTACT | 120 |
| GGCTTCTGGC | CGCGCTCCGG | CCGCGCCTCC | TCTGGATTGC | CCCGAAACAC | CGTGGTACTG | 180 |
| TTGCTGCCGC | AGCAGGAGGC | CTGGGTGGTG | GAGCGAATGG | GCCGATTCCA | CCGGATCCTG | 240 |
| GAGCCTGGTT | TGAACATCCT | CATCCCTGTG | TTAGACCGGA | TCCGATATGT | GCAGAGTCTC | 300 |
| AAGGAAATTG | TCATCAACGT | GCCTGAGCAG | TCGGCTGTGA | CTCTCGACAA | TGTAACCTCTG | 360 |
| CAATTCGATG | GAGTCCTTTA | CCTGCGCATC | ATGGACCCTT | ACAAGGCAAG | CTACGGTGTG | 420 |
| GAGGACCCTG | AGTATGCCGT | CACCCAGCTA | GCTCAAACAA | CCATGAGATC | AGAGCTCGGC | 480 |
| AAACTCTCTN | TGGACAAAGT | CTTCCGGGAA | CGGGAGTCCC | TGAATGCCAG | CATTGTGGAT | 540 |
| GCCATCAACC | AAGCTGCTGA | CTGCTGGGGT | ATCCGCTGCC | TNCGTTATGA | GATCAAGGAT | 600 |
| ATCCATGTGC | CACCCCGGGT | GAAAGAGTCT | ATGCAGATGC | AGGTGGAGGC | AGAGCGGCGG | 660 |
| AAACGGGCCA | CAGTTCTAGA | GTCTGAGGGG | ACCCGAGAGT | CGGCCATCAA | TGTGGCAGAA | 720 |
| GGGAAGAAAC | AGGCCCAGAT | CCTGGCCTCC | GAAGCAGAAA | AGGCTGAACA | GATAAATCAG | 780 |
| GCAGCAGGAG | AGGCCAGTGC | AGTTCTGGCG | AAGGCCAAGG | CTAAAGCTGA | AGCTATTCTGA | 840 |
| ATCCTGGCTG | CAGCTCTGAC | ACAACATAAT | GGAGATGCAG | CAGCTTCACT | GACTGTGGCC | 900 |
| GAGCAGTATG | TCAGCGCGTT | CTCCAAACTG | GCCAAGGACT | CCAACACTAT | CCTACTGCCC | 960 |
| TCCAACCCTG | GCGATGTAC | CAGCATGGTG | GCTCAGGCCA | TGGGTGTATA | TGGAGCCCTC | 1020 |
| ACCAAAGCCC | CAGTGCCAGG | GACTCCAGAC | TCACTCTCCA | GTGGGAGCAG | CAGAGATGTC | 1080 |
| CAGGGTACAG | ATGCAAGTNT | TGATGAGGAA | CTTGATCGAG | TCAAGATGAG | TTAGTGGAGC | 1140 |
| TGGGCTTNGC | CAGGGAGTCT | GGGACAAGG | AAGCAGATTT | TCCTGATT | | 1188 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Genbank
- (B) CLONE: 31069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Lys | Arg | His | Thr | Arg | Asp | Ser | Glu | Ala | Gln | Arg | Leu | Pro |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |
| Asp | Ser | Phe | Lys | Asp | Ser | Pro | Ser | Lys | Gly | Leu | Gly | Pro | Cys | Gly | Trp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ile | Leu | Val | Ala | Phe | Ser | Phe | Leu | Phe | Thr | Val | Ile | Thr | Phe | Pro | Ile |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Ser | Ile | Trp | Met | Cys | Ile | Lys | Ile | Ile | Lys | Glu | Tyr | Glu | Arg | Ala | Ile |
| | | | 50 | | | 55 | | | | | 60 | | | | |
| Ile | Phe | Arg | Leu | Gly | Arg | Ile | Leu | Gln | Gly | Gly | Ala | Lys | Gly | Pro | Gly |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Leu | Phe | Phe | Ile | Leu | Pro | Cys | Thr | Asp | Ser | Phe | Ile | Lys | Val | Asp | Met |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Arg | Thr | Ile | Ser | Phe | Asp | Ile | Pro | Pro | Gln | Glu | Ile | Leu | Thr | Lys | Asp |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Val | Thr | Ile | Ser | Val | Asp | Gly | Val | Val | Tyr | Tyr | Arg | Val | Gln | Asn |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Ala | Thr | Leu | Ala | Val | Ala | Asn | Ile | Thr | Asn | Ala | Asp | Ser | Ala | Thr | Arg |
| | | | 130 | | | 135 | | | | | 140 | | | | |
| Leu | Leu | Ala | Gln | Thr | Thr | Leu | Arg | Asn | Val | Leu | Gly | Thr | Lys | Asn | Leu |
| 145 | | | | | 150 | | | | 155 | | | | | 160 | |
| Ser | Gln | Ile | Leu | Ser | Asp | Arg | Glu | Glu | Ile | Ala | His | Asn | Met | Gln | Ser |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Thr | Leu | Asp | Asp | Ala | Thr | Asp | Ala | Trp | Gly | Ile | Lys | Val | Glu | Arg | Val |
| | | | 180 | | | | 185 | | | | | | 190 | | |
| Glu | Ile | Lys | Asp | Val | Lys | Leu | Pro | Val | Gln | Leu | Gln | Arg | Ala | Met | Ala |
| | | | 195 | | | 200 | | | | | | 205 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Glu | Ala | Glu | Ala | Ser | Arg | Glu | Ala | Arg | Ala | Lys | Val | Ile | Ala | Ala |
| 210 | | | | | | 215 | | | | | 220 | | | | |
| Glu | Gly | Glu | Met | Asn | Ala | Ser | Arg | Ala | Leu | Lys | Glu | Ala | Ser | Met | Val |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ile | Thr | Glu | Ser | Pro | Ala | Ala | Leu | Gln | Leu | Arg | Tyr | Leu | Gln | Thr | Leu |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Thr | Thr | Ile | Ala | Glu | Lys | Asn | Ser | Thr | Ile | Val | Phe | Pro | Leu | Pro | |
| | | | 260 | | | | 265 | | | | | | 270 | | |
| Ile | Asp | Met | Leu | Gln | Gly | Ile | Ile | Gly | Ala | Lys | His | Ser | His | Leu | Gly |
| | 275 | | | | | | 280 | | | | | | 285 | | |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 1065452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Leu | Lys | Thr | Cys | Ser | Leu | Ser | Thr | His | Ser | Phe | Leu | Gln | Lys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Asn | Glu | Lys | His | Asp | Gly | Asn | Pro | Glu | His | Tyr | Asp | Thr | Gly | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Phe | Cys | Gly | Trp | Phe | Leu | Met | Gly | Leu | Ser | Trp | Ile | Met | Val | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Thr | Phe | Pro | Val | Ser | Ile | Tyr | Phe | Cys | Met | Lys | Val | Val | Gln | Glu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Tyr | Glu | Arg | Ala | Val | Ile | Phe | Arg | Leu | Gly | Arg | Leu | Ile | Gly | Gly | Gly |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Ala | Lys | Gly | Pro | Gly | Ile | Phe | Phe | Val | Leu | Pro | Cys | Ile | Glu | Ser | Tyr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Lys | Val | Asp | Leu | Arg | Thr | Val | Ser | Phe | Ser | Val | Pro | Pro | Gln | Glu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ile | Leu | Thr | Lys | Asp | Ser | Val | Thr | Ser | Val | Asp | Ala | Val | Ile | Tyr | |
| | | 115 | | | | | 120 | | | | 125 | | | | |
| Tyr | Arg | Ile | Ser | Asn | Ala | Thr | Val | Ser | Val | Ala | Asn | Val | Glu | Asn | Ala |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| His | His | Ser | Thr | Arg | Leu | Ala | Gln | Thr | Thr | Leu | Arg | Asn | Met | Leu | |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Gly | Thr | Arg | Ser | Leu | Ser | Glu | Ile | Leu | Ser | Asp | Arg | Glu | Thr | Leu | Ala |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Ala | Ser | Met | Gln | Thr | Ile | Leu | Asp | Glu | Ala | Thr | Glu | Ser | Trp | Gly | Ile |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Lys | Val | Glu | Arg | Val | Glu | Ile | Lys | Asp | Val | Arg | Leu | Pro | Ile | Gln | Leu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Gln | Arg | Ala | Met | Ala | Ala | Glu | Ala | Glu | Ala | Thr | Arg | Glu | Ala | Arg | Ala |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Lys | Val | Ile | Ala | Ala | Glu | Gly | Glu | Gln | Lys | Ala | Ser | Arg | Ala | Leu | Arg |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Asp | Ala | Ala | Ser | Val | Ile | Ala | Gln | Ser | Pro | Ala | Ala | Leu | Gln | Leu | Arg |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Tyr | Leu | Gln | Thr | Leu | Asn | Ser | Val | Ala | Arg | Glu | Lys | Phe | Asp | Asp | His |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Leu | Pro | Thr | Ser | Asp | Gly | Ile | Ser | | | | | | | | |
| | | 275 | | | | | 280 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1353669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Tyr | Gly | Met | Pro | Glu | Gly | Ser | Tyr | Asp | Ser | Val | Phe | Thr | Tyr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Pro | Tyr | Asn | Asp | Leu | Asp | Lys | Met | Gly | Tyr | Met | Gly | Pro | Ala | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gln | Gly | Met | Met | Leu | Gly | Asn | Lys | Tyr | Gly | Asn | Phe | Thr | Tyr | Thr | Arg |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asp | Tyr | Gly | Val | Asn | Met | Glu | Asp | Asp | Ile | Lys | Pro | Leu | Ser | Ala | Ile |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Leu | Leu | Ile | Phe | Cys | Val | Ser | Phe | Leu | Phe | Val | Val | Met | Thr | Met |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 |
| Pro | Leu | Ser | Leu | Leu | Phe | Ala | Leu | Lys | Phe | Ile | Ser | Thr | Ser | Glu | Lys |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Leu | Val | Val | Leu | Arg | Leu | Gly | Arg | Ala | Gln | Lys | Thr | Arg | Gly | Pro | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ile | Thr | Leu | Val | Ile | Pro | Cys | Ile | Asp | Thr | Thr | His | Lys | Val | Thr | Met |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ser | Ile | Thr | Ala | Phe | Asn | Val | Pro | Pro | Leu | Gln | Ile | Ile | Thr | Thr | Asp |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Arg | Gly | Leu | Val | Glu | Leu | Gly | Ala | Thr | Val | Phe | Leu | Lys | Ile | Arg | Asp |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Pro | Ile | Ala | Ala | Val | Cys | Gly | Val | Gln | Asp | Arg | Asn | Ala | Ser | Val | Arg |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Thr | Leu | Ala | Asn | Thr | Met | Leu | Tyr | Arg | Tyr | Ile | Ser | Lys | Lys | Arg | Ile |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Cys | Asp | Val | Thr | Ser | Ser | Gln | Asp | Arg | Arg | Ile | Ile | Ser | Ala | Asn | Leu |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Lys | Asp | Glu | Leu | Gly | Ser | Phe | Thr | Cys | Gln | Phe | Gly | Val | Glu | Ile | Thr |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Asp | Val | Glu | Ile | Ser | Asp | Val | Lys | Ile | Val | Lys | Glu | Gly | Glu | Asn | Met |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Gly | Met | Ser | Ala | Leu | Ser | Ser | Val | Ala | Lys | Ser | Asp | Ala | Gly | Gln | Gln |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Leu | Trp | Gln | Val | Ile | Gly | Pro | Val | Phe | Glu | Asp | Phe | Ala | Lys | Glu | Cys |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ala | Ala | Glu | Glu | Lys | Ala | Lys | Glu | Asn | Ala | Pro | Leu | Val | Asp | Leu | Ser |
| | 275 | | | | | | 280 | | | | | | 285 | | |
| Asp | Val | Pro | Ser | Thr | Ser | Ala | Gly | Thr | Ser | Thr | Asp | Thr | Pro | Asn | |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ile | Pro | Ser | Ile | Asp | Ile | Asp | His | Leu | Ile | Ser | Val | Ala | Ser | Leu | Ala |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Met | Asp | Glu | His | Leu | Val | Arg | Leu | Ile | Gly | Arg | Val | Phe | Gln | Ile | Asn |
| | | | 325 | | | | | | 330 | | | | | 335 | |
| Cys | Lys | Asp | Ile | Glu | Pro | Ile | Cys | Ile | Asp | Leu | Lys | His | Gly | Ser | Gly |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Ser | Ala | Tyr | Lys | Gly | Thr | Ser | Leu | Asn | Pro | Asp | Val | Val | Phe | Glu | Thr |
| | 355 | | | | | | 360 | | | | | 365 | | | |
| Ser | Leu | Glu | Val | Phe | Gly | Lys | Ile | Leu | Thr | Lys | Glu | Val | Ser | Pro | Val |

370 375 380
 Thr Val Tyr Met Asn Gly Asn Leu Lys Val Lys Gly Ser Ile Gln Asp
 385 390 395 400
 Ala Met Gln Leu Lys His Leu Val Glu Arg Met Ser Asp Trp Leu
 405 410 415

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Owl
- (B) CLONE: 79701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Gly Ala Val Ala Gly Leu Val Phe Leu Ala Val Leu Val Ile
 1 5 10 15
 Phe Ala Ile Ile Val Val Ala Lys Ser Val Ala Leu Ile Pro Gln Ala
 20 25 30
 Glu Ala Ala Val Ile Glu Arg Leu Gly Arg Tyr Ser Arg Thr Val Ser
 35 40 45
 Gly Gln Leu Thr Leu Leu Val Pro Phe Ile Asp Arg Val Arg Ala Arg
 50 55 60
 Val Asp Leu Arg Glu Arg Val Val Ser Phe Pro Gln Pro Val Ile
 65 70 75 80
 Thr Glu Asp Asn Leu Thr Leu Asn Ile Asp Thr Val Val Tyr Phe Gln
 85 90 95
 Val Thr Val Pro Gln Ala Ala Val Tyr Glu Ile Ser Asn Tyr Ile Val
 100 105 110
 Gly Val Glu Gln Leu Thr Thr Thr Leu Arg Asn Val Val Gly Gly
 115 120 125
 Met Thr Leu Glu Gln Thr Leu Thr Ser Arg Asp Gln Ile Asn Ala Gln
 130 135 140
 Leu Arg Gly Val Leu Asp Glu Ala Thr Gly Arg Trp Gly Leu Arg Val
 145 150 155 160
 Ala Arg Val Glu Leu Arg Ser Ile Asp Pro Pro Pro Ser Ile Gln Ala
 165 170 175
 Ser Met Glu Lys Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Met Ile
 180 185 190
 Leu Thr Ala Glu Gly Thr Arg Glu Ala Ala Ile Lys Gln Ala Glu Gly
 195 200 205
 Gln Lys Gln Ala Gln Ile Leu Ala Ala Glu Gly Ala Lys Gln Ala Ala
 210 215 220
 Ile Leu Ala Ala Glu Ala Asp Arg Gln Ser Arg Met Leu Arg Ala Gln
 225 230 235 240
 Gly Glu Arg Ala Ala Tyr Leu Gln Ala Gln Gly Gln Ala Lys Ala
 245 250 255
 Ile Glu Lys Thr Phe Ala Ala Ile Lys Ala Gly Arg Pro Thr Pro Glu
 260 265 270
 Met Leu Ala Tyr Gln Tyr Leu Gln Thr Leu Pro Glu Met Ala Arg Gly
 275 280 285
 Asp Ala Asn Lys Val Trp Val Val Pro Ser Asp Phe Asn Ala Ala Leu
 290 295 300
 Gln Gly Phe Thr Arg Leu Leu Gly Lys Pro Gly Glu Asp Gly Val Phe
 305 310 315 320
 Arg Phe Glu Pro Ser Pro Val Glu Asp Gln Pro Lys His Ala Ala Asp

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | | | 325 | | | | | | 330 | | | | | | 335 |
| Gly | Asp | Asp | Ala | Glu | Val | Ala | Gly | Trp | Phe | Ser | Thr | Asp | Thr | Asp | Pro | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Ser | Ile | Ala | Arg | Ala | Val | Ala | Thr | Ala | Glu | Ala | Ile | Ala | Arg | Lys | Pro | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Val | Glu | Gly | Ser | Leu | Gly | Thr | Pro | Pro | Arg | Leu | Thr | Gln | | | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1591514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Val | Asn | Asp | Met | Phe | Trp | Phe | Trp | Leu | Ile | Leu | Gly | Ile | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Leu | Phe | Ile | Ile | Val | Lys | Ala | Ile | Val | Ile | Val | Asn | Gln | Tyr | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Gly | Leu | Ile | Phe | Arg | Leu | Gly | Arg | Val | Ile | Gly | Lys | Leu | Lys | Pro |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Ile | Asn | Ile | Ile | Ile | Pro | Phe | Leu | Asp | Val | Pro | Val | Lys | Val | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Met | Arg | Thr | Arg | Val | Thr | Asp | Ile | Pro | Pro | Gln | Glu | Met | Ile | Thr | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Asp | Asn | Ala | Val | Val | Lys | Val | Asp | Ala | Val | Val | Tyr | Tyr | Arg | Val | Ile |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Asp | Val | Glu | Lys | Ala | Ile | Leu | Glu | Val | Glu | Asp | Tyr | Glu | Tyr | Ala | Ile |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ile | Asn | Leu | Ala | Gln | Thr | Thr | Leu | Arg | Ala | Ile | Ile | Gly | Ser | Met | Glu |
| | 115 | | | | | | 120 | | | | | 125 | | | |
| Leu | Asp | Glu | Val | Leu | Asn | Lys | Arg | Glu | Tyr | Ile | Asn | Ser | Lys | Leu | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Glu | Ile | Leu | Asp | Arg | Glu | Thr | Asp | Ala | Trp | Gly | Val | Arg | Ile | Glu | Lys |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Val | Glu | Val | Lys | Glu | Ile | Asp | Pro | Pro | Glu | Asp | Ile | Lys | Asn | Ala | Met |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Ala | Gln | Gln | Met | Lys | Ala | Glu | Arg | Leu | Lys | Arg | Ala | Ala | Ile | Leu | Glu |
| | | | 180 | | | | | 185 | | | | | | 190 | |
| Ala | Glu | Gly | Glu | Lys | Pro | Glu | | | | | | | | | |
| | 195 | | | | | | | | | | | | | | |